

Replacement Sheet

1/7

Figure 1

SEQ ID NO:4 (376-1023)	(1)	ATGCCTGCCTTCAATAGATTGTTTCCCCTGGCTTCTCTCGTGCTTATCTA
SEQ ID NO:3 (363-1010)	(1)	ATGCCTGCCTTCAACAGATTGCTTCCCCTAGCTTCTCTAGTGCTCATCTA
Consensus	(1)	ATGCCTGCCTTCAA AGATTG TTCCCCT GCTTCTCT GTGCT ATCTA
		51 100
SEQ ID NO:4 (376-1023)	(51)	CTGGGTCAGTGCTGCTTCCCTGTGTGTGTGGAAGTGCCTCGGAGACGG
SEQ ID NO:3 (363-1010)	(51)	CTGGGTCAGAGTCTGCTTCCCTGTGTGTGTGGAAGTGCCTCGGAGACAG
Consensus	(51)	CTGGGTCAG GTCTGCTTCCCTGTGTGTGTGGAAGTGCCTCGGAGAC G
		101 150
SEQ ID NO:4 (376-1023)	(101)	AGGCCGTGCAGGGCAACCCCATGAAGCTGCGCTGCATCTCCTGCATGAAG
SEQ ID NO:3 (363-1010)	(101)	AAGCGGTGCAGGGCAATCCCATGAAGCTGAGGTGCATCTCCTGCATGAAG
Consensus	(101)	A GC GTGCAGGGCAA CCCATGAAGCTG G TGCATCTCCTGCATGAAG
		151 200
SEQ ID NO:4 (376-1023)	(151)	AGAGAGGAGGTGGAGGCCACCACGGTGGTGAATGGTTCTACAGGCCCGA
SEQ ID NO:3 (363-1010)	(151)	AGGAGAGGAGGTGGAGGCCACCACGTGGTGGAGTGGTTCTACAGGCCGTA
Consensus	(151)	AG GAGGAGGTGGAGGCCACCAC GTGGTGA TGGTTCTACAGGCC GA
		201 250
SEQ ID NO:4 (376-1023)	(201)	GGGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGCCACCAGGAGG
SEQ ID NO:3 (363-1010)	(201)	GGGCGGTAAAGATTTCCTTATATATGAGTATCGGAATGGCCACCAGGAAG
Consensus	(201)	GGGCGGTAAAGATTTCCTTAT TA GAGTATCGGAATGGCCACCAGGA G
		251 300
SEQ ID NO:4 (376-1023)	(251)	TGGAGAGCCCCCTTTCAGGGGCGCCTGCAGTGAATGGCAGCAAGGACCTG
SEQ ID NO:3 (363-1010)	(251)	TGGAGAGCCCCCTTCCAAGGCCGTCTGCAGTGAATGGGAGCAAAGACCTG
Consensus	(251)	TGGAGAGCCCCCTT CA GG CG CTGCAGTGAATGG AGCAA GACCTG
		301 350
SEQ ID NO:4 (376-1023)	(301)	CAGGACGTGTCCATCACTGTGCTCAACGTCACCTCTGAACGACTCTGGCCT
SEQ ID NO:3 (363-1010)	(301)	CAGGACGTATCCATCACTGTACTCAATGTCACCTTGAATGACTCTGGCCT
Consensus	(301)	CAGGACGT TCCATCACTGT CTCAA GTCAC TGA GACTCTGGCCT
		351 400
SEQ ID NO:4 (376-1023)	(351)	CTACACCTGCAATGTGTCCCGGGAGTTTGAGTTTGAGGCGCATCGGCCCT
SEQ ID NO:3 (363-1010)	(351)	CTACACATGCAATGTGTCCAGGGAGTTTGAATTCGAGGCACACAGGCCTT
Consensus	(351)	CTACAC TGCAATGTGTCC GGGAGTT GA TT GAGGC CA GGCC T
		401 450
SEQ ID NO:4 (376-1023)	(401)	TTGTGAAGACGACGCGCTGATCCCCCTAAGAGTCACCGAGGAGGCTGGA
SEQ ID NO:3 (363-1010)	(401)	TTGTGAAGACCACGAGACTGATACCTTTGCGAGTCACTGAAGAGGCGGGA
Consensus	(401)	TTGTGAAGAC ACG G CTGAT CC T GAGTCAC GA GAGGC GGA
		451 500
SEQ ID NO:4 (376-1023)	(451)	GAGGACTTCACCTCTGTGGTCTCAGAAATCATGATGTACATCCTTCTGGT
SEQ ID NO:3 (363-1010)	(451)	GAAGACTTCACCTCCGTGGTCTCGGAAATCATGATGTACATCCTCCTGGT
Consensus	(451)	GA GACTTCACCTC GTGGTCTC GAAATCATGATGTACATCCT CTGGT
		501 550
SEQ ID NO:4 (376-1023)	(501)	CTTCCTCACCTGTGGCTGCTCATCGAGATGATATATTGCTACAGAAAGG
SEQ ID NO:3 (363-1010)	(501)	CTTCCTCACCTGTGGCTGTTTATTGAGATGATCTATTGCTACAGAAAGG
Consensus	(501)	CTTCCTCACC TGTGGCTG T AT GAGATGAT TATTGCTACAGAAAGG
		551 600
SEQ ID NO:4 (376-1023)	(551)	TCTCAAAAGCCGAAGAGGCAGCCCAAGAAAACGCGTCTGACTACCTTGCC
SEQ ID NO:3 (363-1010)	(551)	TCTCTAAGGCCGAAGAGGCAGCACAGGAAAATGCGTCTGACTACCTTGCT
Consensus	(551)	TCTC AA GCCGAAGAGGCAGC CA GAAA GCGTCTGACTACCTTGCC
		601 648
SEQ ID NO:4 (376-1023)	(601)	ATCCCATCTGAGAACAAGGAGAACTCTGCGGTACCAGTGGAGGAATAG
SEQ ID NO:3 (363-1010)	(601)	ATCCCTTCAGAGAACAAGGAGAACTCTGTGGTACCTGTGGAGGAATAA
Consensus	(601)	ATCCC TC GAGAACAAGGAGAACTCTG GGTACC GTGGAGGAATA

Seq ID No.: 1

Seq ID No.: 2

rat β1

rat P₀

IgV

-20 -10 1 10
 A A'
 MPAFNRL LPLASLVLL YWVRVC FPCVCEVP SETEAV
 MPANRL FPLASLVLL YWVSVC FPCVCEVP SETEAV
 MGTLLALVVGAVLVSSAWG - - - - GCVLEVDS ETEAV
 signal Cleavage site
 I V V Y T D R E V Y G A

Seq ID No.: 1

Seq ID No.: 2

rat β1

rat P₀

IgV

20 30 40
 B B' C
 QGNPMKLR C I SCMKREEVEATT VVE WFYRPEGGKDF
 QGNPMKLR C I SCMKREEVEATT VVE WFYRPEGGKDF
 YGMTFKI L C I SCCKRRSETT AETFT EWTFRQKGT EEF
 VGSQVT L H C S F W S S - E W V S D D I S F T W R Y Q P E G G R D A
 G I h C % h W

Seq ID No.: 1

Seq ID No.: 2

rat β1

rat P₀

IgV

50 60 70
 C' C'' D
 L - I Y E Y R N G H Q E V E S P - - F Q G R L Q W N G S - - - K D L Q D
 L - I Y E Y R N G H Q E V E S P - - F Q G R L Q W N G S - - - K D L Q D
 V K I L R Y E N E V L Q L E E D E R F E G R V V W N G S R G T K D L Q D
 I S I F H Y A K G Q P Y I D E V G T F K E R I Q W V G D - - - P S W K D
 + h

Seq ID No.: 1

Seq ID No.: 2

rat β1

rat P₀

IgV

80 90 100 110
 E F
 V S I T V L N V T L N D S G L Y T C N V S R E F E F E A H R P F V K T T
 V S I T V L N V T L N D S G L Y T C N V S R E F E F E A H R P F V K T T
 L S I F I T N V T Y N H S G D Y E C H V Y R L L F F D N Y E H N T S V V
 G S I V I H N L D Y S D N G T F T C D V K N - - - - P P D I V G K I T
 h h = D # Y C

Seq ID No.: 1

Seq ID No.: 2

rat β1

rat P₀

IgV

120 130 140 150
 G
 R L I P L R V T E E A G E D F T S V V S E I M M Y I L L V F L T L W L F
 R L I P L R V T E E A G E D F T S V V S E I M M Y I L L V F L T L W L L
 K K I H L E V V D K A N R D M A S I V S E I M M Y V L I V V L T I W L V
 T M
 S Q V T L Y V F E
 h h h

Seq ID No.: 1

Seq ID No.: 2

rat β1

160 170 180
 I E M I Y C Y R K V S K A - E E A A Q E N A S D Y L A I P S E N K E N -
 I E M I Y C Y R K V S K A - E E A A Q E N A S D Y L A I P S E N K E N -
 A E M V Y C Y K K I A A A T E A A A Q E N A S E Y L A I T S E S K E N C
 internalization

190

Seq ID No.: 1

Seq ID No.: 2

rat β1

S V V P V E E
 S A V P V E E
 T G V Q V A E

Figure 4